

SEQUENCE LISTING



<110> Cahoon, Rebecca E.
Fang, Yiwen
Odell, Joan
Weng, Zude

<120> Plant Myb Transcription Factor Homologs

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<140> US 10/659,869

<141> 2003-09-11

<150> US 10/021,811

<151> 2001-12-14

<150> US 09/452,244

<151> 1999-12-01

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Val Ser Tyr Ile Ser Gln His Gly Glu Gly Ser Trp Asp Asn Leu Ala
      35             40             45

Arg Ala Ala Gly Leu Asn Arg Asn Gly Lys Ser Cys Arg Leu Arg Trp
      50             55             60

Leu Asn Tyr Leu Arg Pro Gly Val Arg Arg Gly Ser Ile Thr Ala Gly
      65             70             75             80

Glu Asp Thr Val Ile Arg Glu Leu His Ala Arg Trp Gly Asn Lys Trp
      85             90             95

Ser Lys Ile Ser Lys His Leu Pro Gly Arg Thr Asp Asn Glu Xaa Lys
      100            105            110

Asn Tyr Trp Arg Thr Arg Ile Gln Gln Glu Glu Gln Gln Gly Ala Lys
      115            120            125

Thr Thr Gln Gln Arg Asp Arg Xaa Arg Pro Pro Thr Pro Gly Pro Gly
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 Trp Asp Phe Ile Ala Lys Val Ser Gly Leu Asn Arg Thr Gly Lys Ser
 35 40 45
 Cys Arg Leu Arg Trp Val Asn Tyr Leu His Pro Gly Leu Lys Arg Gly
 50 55 60
 Arg Met Ser Pro His Glu Glu Arg Leu Ile Leu Glu Leu His Ala Arg
 65 70 75 80
 Trp Gly Asn Arg Trp Ser Arg Ile Ala Arg Arg Leu Pro Gly Arg Thr
 85 90 95
 Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr His Met Arg Lys Lys Ala
 100 105 110
 Gln Glu Arg Lys Arg Asn Met Ser Pro Ser Ser Ser Ser Ser Leu
 115 120 125
 Ser Tyr Gln Ser Gly Tyr Pro Asp Thr Pro Ser Ile Ile Gly Val Lys
 130 135 140
 Gly Gln Glu Leu His Gly Gly Ser Gly Cys Ile Thr Ser Ile Leu Lys
 145 150 155 160

Gly	Thr	His	Pro	Asp	Met	Asp	Gly	Tyr	Pro	Met	Asp	Gln	Ile	Trp	Met
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Glu Leu Lys

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20	25	30	
Met Leu Leu Val Asn Tyr Val Ala Ala His Gly Glu Gly Arg Trp Asn			
35	40	45	
Ala Leu Ala Arg Cys Ala Gly Leu Arg Arg Thr Gly Lys Ser Cys Arg			
50	55	60	
Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Leu Arg Arg Gly Asn Ile			
65	70	75	80
Thr Ala Gln Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly			
85	90	95	
Asn Arg Trp Ser Xaa Ile Ala Gln His Leu Gln Gly Gln Arg Gln Arg			
100	105	110	
Xaa Xaa Asn Tyr Trp Arg Thr Gly			
115	120		

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gagcagctgc tcatctcgac ctcacaccgc tggggcaacc gatgtcgaag atagcgcanc 480
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35 40 45
Asn Tyr Leu Arg Pro Asp Val Lys Arg Gly Asn Phe Ser Ala Asp Glu
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 35 40 45
 Asp Asn Asn Lys Pro Glu Leu Arg Arg Gly Pro Trp Thr Val Asp Glu
 50 55 60
 Asp Leu Thr Leu Val Asn Tyr Ile Ala Asp Asn Gly Glu Gly Arg Trp
 65 70 75 80
 Asn Asn Leu Ala Arg Ala Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys
 85 90 95
 Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Lys Arg Gly Asn
 100 105 110
 Phe Ser Ala Asp Glu Gln Leu Leu Ile Leu Asp Leu His Thr Arg Trp
 115 120 125
 Gly Asn Arg Trp Ser Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp
 130 135 140
 Asn Glu Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys
 145 150 155 160
 Gln Leu Asn Cys Asp Ala Asn Ser Lys Arg Phe Lys Asp Ala Met Arg
 165 170 175
 Tyr Leu Trp Met Pro His Leu Ala Asp Asp Val Asp Thr Ile Ala Ala
 180 185 190
 Ala Asn Asp Asp Asp Glu Asp His His His Asn Leu Arg Leu Leu Val
 195 200 205
 Leu His His His Gln Ala Gln His Leu Gln Gln Ala Ala Ala Ala Ala
 210 215 220
 Gly Gly Ala Ala Asn Asp Leu Ala Ala Gly Ala Tyr Asp Val Arg Gln
 225 230 235 240
 Leu His Ala Leu Pro Ser Ser Gly Met Ala Ala Thr Ser Ser Ser Asp
 245 250 255
 Ser Leu Ala Ser Glu Ser Tyr Asp Asp Gly Gly Leu Leu Phe Ala Asn
 260 265 270
 Leu Arg Ala Gly Glu Met Leu Met Asp Gly Gly Asp Trp Ala Ala Gln

275 280 285

Gln Glu Ala Asp Gln Gly Leu Trp Pro Pro Pro Pro Pro Pro Ser
 290 295 300

Asp Leu Asp Gln Ser Val Val Gln Ala Ala Gly Ala Gly Ala Gly Gln
 305 310 315 320

Phe Gln Asp Met Glu Leu Ser Gly Trp Val Gln Gly Phe Ser Glu Ser
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 atgtcgatca gatggatgga tgcattgcata tgccgtacat agtagatttg atgatagtaa 180
 ctgacataaaa tataatgtat gcgtgcatc aacgctgggt gttggatcgt ccgtcgtgtg 240
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 20 25 30

Gly Arg Met Ser Pro Glu Glu Glu Arg Met Val Val Gln Leu His Ala
 35 40 45

Lys Leu Gly Asn Arg Trp Ser Arg Ile Ala Lys Ser Ile Pro Gly Arg
 50 55 60

Thr Asp Asn Glu Ile Lys Asn
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<211> 221

<212> PRT

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      20              25              30

Ser Gly Leu Gln Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Val Asn
      35              40              45

Tyr Leu His Pro Gly Leu Lys Arg Gly Arg Met Ser Pro Glu Glu Glu
      50              55              60

Arg Met Val Val Gln Leu His Ala Lys Leu Gly Asn Arg Trp Ser Arg
      65              70              75              80

Ile Ala Lys Ser Ile Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr
      85              90              95

Trp Arg Thr His Leu Arg Lys Leu Lys Leu Lys Gln Gln Lys Gln Gln
      100              105              110

Gln Ser Asp Asp His His Asn Asp Asn Asp Asp Asp Asp Asp Arg Asn
      115              120              125

Ser Ser Ser Ser Ser Ser Ser Ser Asn Ser Asn Ser Asn Leu Gln Gln
      130              135              140

Gln Pro Gln Pro Glu Asp Glu Ser Ser Ala Ser Gly Ser Leu Gln Ala
      145              150              155              160

Gln His His Glu Asp Gln His Gln Leu Phe Leu His Pro Leu Trp Asn
      165              170              175

Asp Asp Ile Ile Val Asp Val Asp Cys Trp Ser Ser Ser Thr Asn Val
      180              185              190

Val Ala Pro Pro Pro Met Pro Ala Ser Pro Leu Trp Asp Ile Asp Asp
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Ala Phe Phe Cys Ser Asp Tyr Ser Leu Pro Leu Trp Gly
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<210> 15
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 acatcccaag cccaatatg gtgacagtga gagaggagat gcgcaaggga ccatggacag 180
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 Glu Asp Leu Gln Leu Val Cys Thr Val Arg Leu Phe Gly Asp Arg Arg
 20 25 30
 Trp Asp Phe Val Ala Lys Val Ser Gly Leu Arg Gly Leu Asn Arg Thr
 35 40 45
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cgtcaactac atcgccgccc atggcgaggg ccgctggaac gcgctcgcg cgtgcgccgg 180
gctgaagcgg acggggaaga gctgccggct gcggtggctg aactacctga ggccggacgt 240
gaggaggggg aacatgacgg cggaggagca gctgctgata ctggagctcc atgggcggtg 300
ggggaatcgg tggagcaaga tcgcgagca tctccccggc cgcaccgaca acgagatcaa 360
gaactactgg cgcaccgcg tccagaagca cgccaagcac ctcaactgcg acgtcaactc 420
ccagcagttc aaggacctca tgcgtacct ctggatgccc gcctcctcga acgcatcaac 480
gctcctccca atccaatcca cgaccgacg acccgactct cgtctccgcc gcacactgat 540
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<213> *Oryza sativa*

<400> 18

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Val Asn Tyr Ile Ala Ala His Gly Glu Gly Arg Trp Asn Ala Leu Ala
      35             40             45

Arg Cys Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp
      50             55             60

Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Met Thr Ala Glu
      65             70             75             80

Glu Gln Leu Leu Ile Leu Glu Leu His Gly Arg Trp Gly Asn Arg Trp
      85             90             95

Ser Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys
      100            105            110

Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys His Leu Asn Cys
      115            120            125

Asp Val Asn Ser Gln Gln Phe Lys Asp Leu Met Arg Tyr Leu Trp Met
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Pro
145
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<213> *Oryza sativa*

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tcccgatggg gcaaccgatg gtccaagata gcacaacatt tgcctgggag gaccgacgac 180
gagatcaaga actactggag gaccagagtg caaaagcatg ccaagcaact caattgtgat 240
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 cgcattccatg ccagggctgg cgctgttgat gatagcggag actacagcaa caacgactta 360
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 <213> Oryza sativa

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 20 25 30
 Gln Leu Leu Ile Leu Asp Leu His Ser Arg Trp Gly Asn Arg Trp Ser
 35 40 45
 Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asp Glu Ile Lys Asn
 50 55 60
 Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu Asn Cys Asp
 65 70 75 80
 Val Asn Ser Lys Arg Phe Lys Asp Ala Met Lys Tyr Leu Trp Met Pro
 85 90 95
 Arg Leu Ala Glu Arg Ile His Ala Arg Ala Gly Ala Val Asp Asp Ser
 100 105 110
 Gly Asp Tyr Ser Asn Asn Asp Leu Ser Cys Val Ser Gly Val Thr Met
 115 120 125
 Ala Thr Val Ala Asn Cys Phe Asp Gly Ser Pro Ser Met Val Thr Ser
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 tctatccgat caatcgactg gcccgcgagg atcgatcgag actcgaaaagg gagggatttt 180
 gatccggatc ggtcgacgat ggacatggcg cagcagaggg acgcgagcag cgaggaggag 240
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 aactacatcg ccgcgcacgg cgagggccgc tggaaactcg tcgcccgatc agcanggctg 360
 aaacgcacag gcaagagctg ccggctccgg tggctgaact acctccgccc cgacctccgg 420
 cgaggcaaca tcacgccgca agagcagctg ctcatcctgg agctgcactc gcggtgggga 480
 aaccgctggt ccaagatngc gcagcacctc ccgggaagca ccgacaacga gatnaagaat 540
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 aggacncatg cgctactcng gatgcccgct ctnagggat 640

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Gly	Gly	Asp	Leu	Arg	Arg	Gly	Pro	Trp	Thr	Val	Glu	Glu	Asp	Leu	Leu
		20					25						30		

Leu	Val	Asn	Tyr	Ile	Ala	Ala	His	Gly	Glu	Gly	Arg	Trp	Asn	Ser	Leu
		35					40					45			

Ala	Arg	Ser	Ala	Xaa	Leu	Lys	Arg	Thr	Gly	Lys	Ser	Cys	Arg	Leu	Arg
	50					55					60				

Trp	Leu	Asn	Tyr	Leu	Arg	Pro	Asp	Leu	Arg	Arg	Gly	Asn	Ile	Thr	Pro
65					70					75					80

Gln	Glu	Gln	Leu	Leu	Ile	Leu	Glu	Leu	His	Ser	Arg	Trp	Gly	Asn	Arg
			85						90					95	

Trp	Ser	Lys	Xaa	Ala	Gln	His	Leu	Pro	Gly	Ser	Thr	Asp	Asn	Glu	Xaa
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Lys	Asn	Thr
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 cggcaactgg cgcgccgtgc cgacgaacac cgggctgatg cgttgagca agagctgccg 240
 gctccgggtgg acgaactacc tcaggccggg gatcaagcgg gggaacttca ccgagcanga 300
 ggagaagctc atcgctccacc tccaggctct cctcggcaac cgggtgggcaa cgatnncgtc 360
 gtacttgccg gganangacg ncaacnacat cangaatact gggaacannc acctcangaa 420
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35						40						45					
Cys	Ser	Lys	Ser	Cys	Arg	Leu	Arg	Trp	Thr	Asn	Tyr	Leu	Arg	Pro	Gly		
50						55				60							
Ile	Lys	Arg	Gly	Asn	Phe	Thr	Glu	Xaa	Glu	Glu	Lys	Leu	Ile	Val	His		
65				70						75		80					
Leu	Gln	Ala	Leu	Leu	Gly	Asn	Arg	Trp	Ala	Thr	Xaa	Xaa	Ser	Tyr	Leu		
			85						90			95					
Pro	Gly	Xaa	Asp	Xaa	Asn	Xaa	Ile	Xaa	Asn	Thr	Gly	Asn	Xaa	His	Leu		
			100						105			110					
Xaa	Lys	Asn	Ser	Arg	Xaa	Cys	Lys	Pro	Pro	Glu	Val	Xaa	Lys				
115						120						125					

20					25					30					
Gly	Ala	Gly	Asn	Trp	Arg	Ala	Val	Pro	Thr	Asn	Thr	Gly	Leu	Met	Arg
		35					40					45			
Cys	Ser	Lys	Ser	Cys	Arg	Leu	Arg	Trp	Thr	Asn	Tyr	Leu	Arg	Pro	Gly
	50					55					60				
Ile	Lys	Arg	Gly	Asn	Phe	Thr	Glu	Gln	Glu	Glu	Lys	Leu	Ile	Val	His
65					70					75					80
Leu	Gln	Ala	Leu	Leu	Gly	Asn	Arg	Trp	Ala	Ala	Ile	Ala	Ser	Tyr	Leu
				85					90					95	
Pro	Glu	Arg	Thr	Asp	Asn	Asp	Ile	Lys	Asn	Tyr	Trp	Asn	Thr	His	Leu
			100					105					110		
Lys	Lys	Lys	Leu	Lys	Lys	Met	Gln	Ala	Ala	Gly	Gly	Gly	Glu	Asp	Ser
		115					120					125			
Gly	Ala	Ala	Ser	Glu	Gly	Gly	Gly	Gly	Arg	Gly	Asp	Gly	Asp	Gly	Gly
	130					135					140				
Gly	Lys	Ser	Val	Lys	Ala	Ala	Ala	Pro	Lys	Gly	Gln	Trp	Glu	Arg	Arg
145					150					155					160
Leu	Gln	Thr	Asp	Ile	His	Thr	Ala	Arg	Gln	Ala	Leu	Arg	Asp	Ala	Leu
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Ser	Leu	Asp	His	Pro	Asp	Pro	Ser	Pro	Ala	Thr	Ala	Ala	Ala	Ala	Ala
			180					185					190		
Thr	Pro	Ala	Gly	Ser	Ser	Ala	Ala	Tyr	Ala	Ser	Ser	Ala	Asp	Asn	Ile
		195						200					205		
Ala	Arg	Leu	Leu	Gln	Gly	Trp	Met	Arg	Pro	Gly	Gly	Gly	Gly	Gly	Gly
	210					215					220				
Asn	Gly	Lys	Gly	Pro	Glu	Ala	Ser	Gly	Ser	Thr	Ser	Thr	Thr	Ala	Thr
225					230					235					240
Thr	Gln	Gln	Gln	Pro	Gln	Cys	Ser	Gly	Glu	Gly	Ala	Ala	Ser	Ala	Ser
				245					250					255	
Ala	Ser	Ala	Ser	Gln	Ser	Gly	Ala	Ala	Ala	Ala	Ala	Thr	Ala	Gln	Thr
			260				265						270		
Pro	Glu	Cys	Ser	Thr	Glu	Thr	Ser	Lys	Met	Ala	Thr	Gly	Gly	Gly	Ala
		275					280					285			
Gly	Gly	Pro	Ala	Pro	Ala	Phe	Ser	Met	Leu	Glu	Ser	Trp	Leu	Leu	Asp
	290					295					300				
Asp	Gly	Gly	Met	Gly	Leu	Met	Asp	Val	Val	Pro	Leu	Gly	Asp	Pro	Ser
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Glu	Phe	Phe													

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attnagcaac aatcacataa ctctgagata atgttacaag ctagatacca agttntacaa 480
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      20                      25                      30
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Asn Ser Leu Ala Lys Ser Cys Trp Ser Gln Thr Tyr Arg Lys Asp Cys
      35                      40                      45
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Arg Leu Xaa Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn
      50                      55                      60
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Xaa Thr Pro Glu Gly Thr Thr Leu Ile Met Glu Leu His Ala Lys Trp
65 70 75 80

Asn Arg Trp Ser Lys Ile Ala Lys His Leu Pro Gly Arg Thr
85 90

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acgatggaag aagacttgat cttgatcaac tatattgcaa atcatgggga aggtgtttgg 180
aattcttttg ccaaagctgc tggctctcaa cgtaccggaa agagttgccg gctaagggtg 240
ctaaactacc tccgtcctga tgtagaaga gggaatatta cacccgagga acaacttttg 300
atcatggagc ttcacgcaaa gtggggaaac aggtgggtcca aaattgcca gcacatcaag 360
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caagctgaga actttcagca acaaactcagc aataactctg agataaatga tcaccaagct 480
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caaggaatgt tagagccatt ttcttcaatt cagttcccca caattaatcc tgatcaatcc 600
agttgttgta ccaatgacaa caacaacagc attaatatt ggagcatgga ggatatctgg 660
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tataagttcc ataaaacact ggaatgtctc tggcttaaaa catattatta ttaggtttgt 780
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35 40 45
Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu
50 55 60
Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu
65 70 75 80
Ile Met Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala
85 90 95
Lys His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg
100 105 110
Thr Arg Ile Gln Lys His Ile Lys Gln Ala Glu Asn Phe Gln Gln Gln
115 120 125

Ile	Ser	Asn	Asn	Ser	Glu	Ile	Asn	Asp	His	Gln	Ala	Ser	Thr	Ser	His
130						135				140					
Val	Ser	Thr	Met	Ala	Glu	Pro	Met	Glu	Thr	Tyr	Ser	Pro	Pro	Phe	Tyr
145					150					155					160
Gln	Gly	Met	Leu	Glu	Pro	Phe	Ser	Ser	Ile	Gln	Phe	Pro	Thr	Ile	Asn
				165					170					175	
Pro	Asp	Gln	Ser	Ser	Cys	Cys	Thr	Asn	Asp	Asn	Asn	Asn	Ser	Ile	Asn
			180					185					190		
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 tggaaactctt tggccaaggc tgctggactt aaacgtaccg gaaagagttg ccggctccgg 180
 tggctaaact acctccgtcc tgatgttaga agaggggaata ttacaccgga ggaacagctt 240
 ttgatcatgg aacttcatgc aaagtgggga aacaggtggt ccaaaaattgc caagcatcta 300
 nccggaagga ctgataatga gattaagaac tactggagga caaggatcaa gaacantca 360
 agcaagcctt caacaacttc aacaacanag tantaattct gagataattt acatcccaag 420
 cttgcacaac caattgtcaa caatggggcaa ccaaaaaaaa ctaatctcan caatttcaag 480
 gaagnttatt cattnaatca attccaaaaa ccncacntct antgtttcaa 530

<210> 32
 <211> 204
 <212> PRT
 <213> Glycine max

<400> 32
 Met Asp Lys Lys Leu Gly Asn Thr Ser His Asp Pro Glu Val Arg Lys
 1 5 10 15
 Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Thr Tyr Ile Ala
 20 25 30
 Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly Leu
 35 40 45
 Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg
 50 55 60
 Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile
 65 70 75 80
 Met Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys
 85 90 95
 His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr
 100 105 110
 Arg Ile Gln Lys His Leu Lys Gln Ala Ser Ser Ser Phe Gln Gln Gln
 115 120 125
 Ser Ser Asn Ser Glu Ile Ile Tyr His Pro Gln Ala Cys Thr Ser Gln
 130 135 140
 Val Ser Thr Met Ala Gln Pro Ile Glu Thr Tyr Ser Pro Pro Ser Tyr
 145 150 155 160
 Gln Gly Met Leu Asp Pro Phe Ser Ile Gln Phe Pro Thr Asn Pro His
 165 170 175
 His Ser Ser Cys Cys Thr Asn Asp Asp Asp Asn Asn Asn Tyr Trp Ser
 180 185 190

Met Glu Asp Ile Trp Ser Met Gln Leu Ala Asn Tyr
 195 200

<210> 33
 <211> 910
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (798)
 <223> n is a, c, g or t

<220>
 <221> unsure
 <222> (807)
 <223> n is a, c, g or t

<220>
 <221> unsure
 <222> (814)
 <223> n is a, c, g or t

<400> 33
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 aactatattg caaatcacgg tgaagggtgt tgggaattctt tagccaaagc ttctgggtctt 180
 aaacgaacgg gaaagagttg tcgactccgt tggctaaact accttcgtcc tgatgttaga 240
 agaggaaaca ttacaccoga agaacagctt ttgatcatag aacttcattg aaagtggggc 300
 aataggtggt ccaaaattgc aaagcatctt ccaggaagaa ctgacaatga gattaagaac 360
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 aattcatcag agaatagtaa taatgatcat caagcaagca atagcactag caaggtgtcc 480
 accatggcac atccaaatga gactttctct tcaccctcat accaagcaac ttttgagcca 540
 tttcaacctc aattcctaca atcaatgatc aatcaagttg ttgtaccagc aacaacaact 600
 attggagcat cgaggatatc tggtcgtcta tgcaattact caatggagat waattaaatc 660
 tagctatatg catgcttata taaatcatat atgtgatgat atataaacct aagctcttat 720
 tgagtgtggt caggcttaat aacatcatta ggtctggtat atatgagtag gttaagattg 780
 gtgtgcatgc ctaaattgnag tattgcntta ttgnagtaag aataactagt tatggatgcc 840
 tttaaaaaaa agttagttat gaattgaaat atatagtaac ttatatacta aaaaaaaaaa 900
 aaaaaaaaaa 910

<210> 34
 <211> 206
 <212> PRT
 <213> Glycine max

<400> 34
 Met Asp Lys Lys Pro Cys Asp Ser Ser His Asp Pro Glu Val Arg Lys
 1 5 10 15
 Gly Pro Trp Ile Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile Ala
 20 25 30
 Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ser Gly Leu
 35 40 45
 Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg
 50 55 60
 Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile

65		70		75		80
Ile Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys						
	85			90		95
His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Arg Thr						
	100			105		110
Arg Ile Gln Lys His Ile Lys Gln Ala Glu Thr Ser Gln Gln His Gly						
	115			120		125
Asn Ser Ser Glu Asn Ser Asn Asn Asp His Gln Ala Ser Asn Ser Thr						
	130			135		140
Ser Lys Val Ser Thr Met Ala His Pro Asn Glu Thr Phe Ser Ser Pro						
	145			150		155
Ser Tyr Gln Ala Thr Phe Glu Pro Phe Gln Pro Gln Phe Leu Gln Ser						
	165			170		175
Met Ile Asn Gln Val Val Val Pro Ala Thr Thr Thr Ile Gly Ala Ser						
	180			185		190
Arg Ile Ser Gly Arg Leu Cys Asn Tyr Ser Met Glu Ile Asn						
	195			200		205

<210> 35
 <211> 863
 <212> DNA
 <213> Glycine max

<400> 35
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 tattgcaaat catggggaag gtgtttggaa ctctttggcc aaagctgctg gtctcaaacg 180
 taacggaaag agttgccggc taagggtggct aaattacctc cgtcctgatg ttagaagagg 240
 gaatattaca cccgaggaac aacttttgat tatggagctc cagcgaaggt ggggaaacag 300
 gtgggtccaaa attgccaagc atctacctgg aaggactgat aatgagatca agaactattg 360
 gaggacaagg atccagaagc acatcaagca agctgagaac tttcagcaac agagtagtaa 420
 taattctgag ataaatgatc accaagctag cactagccat gtttccacca tggctgagcc 480
 catggagatg tattctccac cctgttatca aggaatgtta gagccatttt caactcagtt 540
 ccctacaatt aatcctgatc aatccagttg ttgtaccaat gacaacaaca acattaacta 600
 ttggagcatg gaggatagct ggtcaatgca attactgaac ggtgattaaa tattatcaag 660
 ataaaaccta agttypgaag ttccataagg ctggaatgtc tytgatttaa aacatattat 720
 tgggtttggt tatataagta gttggatgtt tgggtttgcg taccattatt agctatgtgc 780
 tgtaatatat acgagatytt atattaaact atatctgcat gctttatata taaaaaaaaa 840
 aaaaaaaaaa aaaaaaaaaa aaa 863

<210> 36
 <211> 206
 <212> PRT
 <213> Glycine max

<400> 36
Met Asp Lys Lys Gln Gln Cys Lys Thr Ser Gln Asp Pro Glu Val Arg
1 5 10 15
Lys Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Met Asn Tyr Ile
20 25 30
Ala Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly

35	40	45
Leu Lys Arg Asn Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu		
50	55	60
Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu		
65	70	75
Ile Met Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala		
	85	90
Lys His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg		
	100	105
Thr Arg Ile Gln Lys His Ile Lys Gln Ala Glu Asn Phe Gln Gln Gln		
	115	120
Ser Ser Asn Asn Ser Glu Ile Asn Asp His Gln Ala Ser Thr Ser His		
	130	135
Val Ser Thr Met Ala Glu Pro Met Glu Met Tyr Ser Pro Pro Cys Tyr		
145	150	155
Gln Gly Met Leu Glu Pro Phe Ser Thr Gln Phe Pro Thr Ile Asn Pro		
	165	170
Asp Gln Ser Ser Cys Cys Thr Asn Asp Asn Asn Asn Ile Asn Tyr Trp		
	180	185
Ser Met Glu Asp Ser Trp Ser Met Gln Leu Leu Asn Gly Asp		
	195	200
		205

<210> 37
 <211> 805
 <212> DNA
 <213> Glycine max

<400> 37
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 ttagccaaag cttctgggtct caaacgaacg ggaaagagtt gtcgactccg ttggctaaac 180
 taccttcgtc ctgatgttag aagaggaaac attacacccg aggaacagct tttgatcata 240
 gaacttcatg caaagtgggg caataggtgg tccaaaattg caaagcatct tccaggaaga 300
 actgacaatg agattaagaa cttctggaga acaaggatcc aaaagcacat taagcaagct 360
 gagacttcac aacaacatgg taattcagag aataatgatc atcaagcaag cactagtact 420
 agcaaagtgt ccaccatggc acatccaaat gagactttct ctccaccctc ataccaagga 480
 acttttgagc cattccaacc tcaattccct acaatcactg atcaatcaag ttgttggtacc 540
 accaccaacg acaacaacaa ctattggagc atcgaggata tctggtcgtc tatgcaatta 600
 ctcaatggag attaaacctt gctatatgca tgcctatata aatcatatat atgatgatat 660
 ataaacctaa gctctttagt agtgtgttca ggcttaataa catcattagg tctgtttata 720
 tgagtagtct aagtttggtg tttgtaatgc atgatgtgag ttaagaatta atttagttat 780
 gggttgaaaa aaaaaaaaaa aaaaa 805

<210> 38
 <211> 204
 <212> PRT
 <213> Glycine max

<400> 38
 Lys Lys Pro Cys Asn Ser Ser Ser His Asp Pro Glu Val Arg Lys Gly
 1 5 10 15

Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile Ala Asn
 20 25 30
 His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ser Gly Leu Lys
 35 40 45
 Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro
 50 55 60
 Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile Ile
 65 70 75 80
 Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys His
 85 90 95
 Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Arg Thr Arg
 100 105 110
 Ile Gln Lys His Ile Lys Gln Ala Glu Thr Ser Gln Gln His Gly Asn
 115 120 125
 Ser Glu Asn Asn Asp His Gln Ala Ser Thr Ser Thr Ser Lys Val Ser
 130 135 140
 Thr Met Ala His Pro Asn Glu Thr Phe Ser Pro Pro Ser Tyr Gln Gly
 145 150 155 160
 Thr Phe Glu Pro Phe Gln Pro Gln Phe Pro Thr Ile Thr Asp Gln Ser
 165 170 175
 Ser Cys Cys Thr Thr Thr Asn Asp Asn Asn Asn Tyr Trp Ser Ile Glu
 180 185 190
 Asp Ile Trp Ser Ser Met Gln Leu Leu Asn Gly Asp
 195 200

<210> 39
 <211> 751
 <212> DNA
 <213> Glycine max

<400> 39
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 aaaaggagat gggcatgaga aaaggtccat gggcggttga ggaggacacc attctggtca 120
 attacatcgc cacacacggt gaaggccact ggaattccgt ggcacgatgt gcaggtctaa 180
 ggaggagtgg gaagagttgc agattaaggt ggctaaacta cttgcgcca gacgtgcggc 240
 gtggaaatat cacactccaa gaacaaatat taattctcga ccttcaactct cgctggggca 300
 acaggtggtc aaagattgct caacagctgc caggaagaac agacaacgaa ataaagaact 360
 attggaggac cagagtgata aaacaagcga agcagctaaa gtgcgatgtg aatagcaaac 420
 agttcagaga cacgttgctg tacgtttgga tgccgcgctt gctggagcgg cttcagccca 480
 catcacaagc actggagcca aaccaaagtg gacttgtgtt acacgcttca tcatcactgc 540
 ttccttcgaa ttccgaccat agtattgaaa gggggtcgga tctgtggcca ggtttcaata 600
 accaaatggt gttggaacag gggagtggcg gtgacttgtt ggaaagtgtg tgggatgacg 660
 acaatatgtg ctttttgcaa cagctttctt atgacctcca aatgaaataa aatacaattc 720
 ctttccgtca cgcaaaaaaa aaaaaaaaaa a 751

<210> 40
 <211> 235
 <212> PRT
 <213> Glycine max

<400> 40

Asp Val Lys Lys Gly Gly Ser Val Val Gln Ala Gln Val Lys Leu Gln
1 5 10 15
Lys His Asn Glu Lys Glu Met Gly Met Arg Lys Gly Pro Trp Ala Val
20 25 30
Glu Glu Asp Thr Ile Leu Val Asn Tyr Ile Ala Thr His Gly Glu Gly
35 40 45
His Trp Asn Ser Val Ala Arg Cys Ala Gly Leu Arg Arg Ser Gly Lys
50 55 60
Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg
65 70 75 80
Gly Asn Ile Thr Leu Gln Glu Gln Ile Leu Ile Leu Asp Leu His Ser
85 90 95
Arg Trp Gly Asn Arg Trp Ser Lys Ile Ala Gln Gln Leu Pro Gly Arg
100 105 110
Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr Arg Val Ile Lys Gln
115 120 125
Ala Lys Gln Leu Lys Cys Asp Val Asn Ser Lys Gln Phe Arg Asp Thr
130 135 140
Leu Arg Tyr Val Trp Met Pro Arg Leu Leu Glu Arg Leu Gln Pro Thr
145 150 155 160
Ser Gln Ala Leu Glu Pro Asn Gln Ser Gly Leu Val Leu His Ala Ser
165 170 175
Ser Ser Leu Leu Pro Ser Asn Ser Asp His Ser Ile Glu Arg Gly Ser
180 185 190
Asp Leu Trp Pro Gly Phe Asn Asn Gln Met Leu Leu Glu Gln Gly Ser
195 200 205
Gly Gly Asp Leu Leu Glu Ser Leu Trp Asp Asp Asp Asn Met Cys Phe
210 215 220
Leu Gln Gln Leu Ser Tyr Asp Leu Gln Met Lys
225 230 235

<210> 41

<211> 500

<212> DNA

<213> Glycine max

<400> 41

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gagtgaagctg agaagaggtc cttggactct tgaagaagac agcttactca tacactatat 180
tgctcgtcat ggtgaaggcc gttggaatat gttagccaaa agtgcaggat tgaagaggac 240
tggaaaaagt tgcagactta gatggctgaa ttatttgaaa ccagacatta agagagggaa 300
cctcactcca caggagcaac tcttgatcct tgaactccat tccaagtggg gtaacagggtg 360
gtcaaaaatt gctcagcatc tgccaggaag aacagacaat gagatcaaga actattggag 420
aacaaggata cagaaacagg gcacgccaac ttaacattga atctggtagc aagagattca 480

ttgatgctgt cagtgttttt

500

<210> 42

<211> 229

<212> PRT

<213> Glycine max

<220>

<221> UNSURE

<222> (138)

<223> Xaa can be any naturally occurring amino acid

<400> 42

Met Ser Thr Ile Ala Lys Arg Asp Leu Ser Ser Asn Glu Glu Glu Ser
1 5 10 15

Glu Leu Arg Arg Gly Pro Trp Thr Leu Glu Glu Asp Ser Leu Leu Ile
20 25 30

His Tyr Ile Ala Arg His Gly Glu Gly Arg Trp Asn Met Leu Ala Lys
35 40 45

Ser Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu
50 55 60

Asn Tyr Leu Lys Pro Asp Ile Lys Arg Gly Asn Leu Thr Pro Gln Glu
65 70 75 80

Gln Leu Leu Ile Leu Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser
85 90 95

Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn
100 105 110

Tyr Trp Arg Thr Arg Ile Gln Lys Gln Ala Arg Gln Leu Asn Ile Glu
115 120 125

Ser Gly Ser Lys Arg Phe Ile Asp Ala Xaa Lys Cys Phe Trp Met Pro
130 135 140

Arg Leu Leu Gln Lys Met Glu Gln Ser Asn Ser Pro Ser Pro His His
145 150 155 160

Ser Ser Met Thr Asn Met Met Asn Leu Gly Asn Ser Gly Glu Ala Ser
165 170 175

Met Ser Ser Met Ser Ser Ser Phe Asn Ile Asn Pro Ser Met Ser Ser
180 185 190

Ser Ser Ser Pro Pro Lys Gly Asn Leu Leu Trp Met Met Pro Asn His
195 200 205

Phe Lys Tyr Tyr Val Gln Pro His Gln Ser Ile Pro Arg Phe Leu Pro
210 215 220

Ile Phe Thr Ala Thr
225

<210> 43

<211> 1348

<212> DNA

<213> Glycine max

<400> 43

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tatcaattac gttgccactc atggcgaagg tcgctggaat accctcgccc tctctgctgg 240
gctgaaacga acggggaaga gttgcagatt gaggtggctg aattatctgc gtcctgatgt 300
tcgacgtgga aacatcacgc ttgaagaaca acttttgatt ctggagctcc attctcgctg 360
gggaaaccga tggtcgaaaa ttgctcaata tttgcctggt agaaccgaca atgagataaa 420
gaactattgg agaaccctg tccaaaagca tgccaagcaa ctcaaatgcg acgtgaatag 480
caagcaattc aaggacacca tgcgttacat ttggatgcca aggctcgtgg aacgcattca 540
agccaccgct gccgcctccg caccacaacc cgttaccgta ccaccgcgac caacaatgca 600
tacacctacg gaagcaacct taataacaac aaattcgagg ttcacgatca caagggcaaa 660
atgggggttaa ccgatccttc agttatgaac aatgacttaa tgggttcaca tgtcacgcaa 720
agttacaccc ctgagaatag tagcaccggt gcgtcatcat cagactcgtt tgggactcaa 780
gtctcagcaa tttctgattt gactgaatat tacactgtca ctggtagtgg taacaataac 840
aatactaatt ctgcggtatta ttatcaaccc tctcaaatta gttactcgga tagttgcatc 900
acaagcccat ctgggttggt ccctcaaggg ctagattttc aatccatgga tccaaacacc 960
ccgtggaaca tgcaaagtgg ggactcctct gacagttttt ggaacgttga aagcatgttg 1020
ttcttagagc agcaactcat gaatgacaac atgtgaaaac attgggaata ggaaaataag 1080
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ttttattctt ttatgaatta tgaattagat tgacagaagg ggttgtttgt gaaatataca 1260
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<210> 44

<211> 196

<212> PRT

<213> Glycine max

<400> 44

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Met Asp Gly Lys Gly Ala Arg Ser Ser Asn Thr Leu Leu Ser Ser Glu
 1                5                10                15

Asp Glu Met Asp Leu Arg Arg Gly Pro Trp Thr Val Asp Glu Asp Leu
20                25                30

Thr Leu Ile Asn Tyr Val Ala Thr His Gly Glu Gly Arg Trp Asn Thr
35                40                45

Leu Ala Leu Ser Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu
50                55                60

Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr
65                70                75                80

Leu Glu Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn
85                90                95

Arg Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu
100               105               110

Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu
115               120               125

Lys Cys Asp Val Asn Ser Lys Gln Phe Lys Asp Thr Met Arg Tyr Ile
130               135               140

Trp Met Pro Arg Leu Val Glu Arg Ile Gln Ala Thr Ala Ala Ala Ser
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[illegible]

<400> 45						
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gcaacaccct	tttaagttgt	gaggacgaga	tggaacctcg	aagaggccct	tggaaccgtcg	180
atgaagacct	cactcttatc	aattacattg	ccactcatgg	cgaaggctcg	tggaacacgc	240
tcgcccctct	tgctgggctg	aaacgaacgg	ggaagagttg	cagattgagg	tggtctgaatt	300
atctgcgtcc	tgatgttcga	cgtggaaaca	tcacacattg	agaacaactt	ttgattctgg	360
agcttcattc	tcgctggggg	aaccgttggt	cgaaaaattg	tcaatathtt	cctggttagaa	420
ccgacaacga	gataaagaac	tattggagaa	cccggtgcc	aaagcatgcc	aagcaactca	480
aactgtgacgt	gaatagcaag	caattcaagg	acaccatgng	ntacctttgn	natnccaagg	540

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ctcgtggaac gcattcaagc agcggcgacg gcccccgtaa ccaccaccgt aactgcggcc 600
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atcacaaggg cagaatgggg ttaaccgata cttcagttgc gaacaatgac tttgtggggt 720
cacatgtcac gcaaaggtag cctactcctg agaatagtag cacgggtgcg tcatcatcag 780
actcgtttgg gactcaagtn tcaacaattt ctgatttgac tgaaaattcc agtgtccctg 840
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gcatcacaag cccatctggg ttcttggttc ctcaaggact agatcttcaa tccatggatc 960
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<210> 46
<211> 322
<212> PRT
<213> Glycine max

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<220>
<221> UNSURE
<222> (142)
<223> Xaa can be any naturally occurring amino acid

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<220>
<221> UNSURE
<222> (145)..(146)..(147)
<223> Xaa can be any naturally occurring amino acid

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<220>
<221> UNSURE
<222> (178)
<223> Xaa can be any naturally occurring amino acid

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<400> 46
Met Asp Glu Lys Gly Ala Arg Ser Ser Asn Thr Leu Leu Ser Cys Glu
 1             5             10             15

Asp Glu Met Asp Leu Arg Arg Gly Pro Trp Thr Val Asp Glu Asp Leu
      20             25             30

Thr Leu Ile Asn Tyr Ile Ala Thr His Gly Glu Gly Arg Trp Asn Thr
      35             40             45

Leu Ala Leu Ser Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu
      50             55             60

Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr
      65             70             75             80

Leu Glu Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn
      85             90             95

Arg Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu
      100            105            110

Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu
      115            120            125

Lys Cys Asp Val Asn Ser Lys Gln Phe Lys Asp Thr Met Xaa Tyr Leu
      130            135            140

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Xaa	Xaa	Xaa	Lys	Ala	Arg	Gly	Thr	His	Ser	Ser	Ser	Gly	Asp	Gly	Pro
145					150					155					160
Arg	Asn	His	His	Arg	Asn	Cys	Gly	Arg	His	Gln	Gln	Cys	Ile	His	Leu
				165					170					175	
Arg	Xaa	Gln	Pro	Tyr	Thr	Thr	Lys	Phe	Glu	Val	Leu	Asn	His	Lys	Gly
			180					185						190	
Arg	Met	Gly	Leu	Thr	Asp	Pro	Ser	Val	Ala	Asn	Asn	Asp	Phe	Val	Gly
		195					200					205			
Ser	His	Val	Thr	Gln	Arg	Tyr	Pro	Thr	Pro	Glu	Asn	Ser	Ser	Thr	Gly
	210					215					220				
Ala	Ser	Ser	Ser	Asp	Ser	Phe	Gly	Thr	Gln	Val	Ser	Thr	Ile	Ser	Asp
225					230					235					240
Leu	Thr	Glu	Asn	Ser	Ser	Val	Pro	Glu	Asn	Thr	Asn	Ser	Ala	Asp	Tyr
				245					250					255	
Tyr	Gln	Pro	Ser	Gln	Ile	Ser	Asn	Tyr	Ser	Asp	Asn	Cys	Ile	Thr	Ser
			260					265						270	
Pro	Ser	Gly	Phe	Leu	Phe	Pro	Gln	Gly	Leu	Asp	Leu	Gln	Ser	Met	Asp
		275					280					285			
Pro	Asn	Thr	Pro	Trp	Asn	Met	Gln	Ser	Gly	Asp	Ser	Ser	Asp	Asn	Phe
	290					295					300				
Trp	Asp	Val	Glu	Ser	Met	Leu	Phe	Leu	Glu	Gln	Gln	Leu	Met	Asn	Asp
305					310					315					320

Asn Met

<210> 47
 <211> 1181
 <212> DNA
 <213> Glycine max

<400> 47

tttcagt	tgagaat	catgtct	tcaaagag	tcagcag	tagtgaag	60
gacaatg	ttagaag	gccttgg	ctggaag	ataactt	ctcccaat	120
attttta	atgggga	gcgatgg	ttgctgg	aacgttc	attaaaga	180
actggga	gttcag	aaggtgg	aattatc	agccaga	aaaacggg	240
aattta	cacaaga	acttata	cttgaac	actcaa	gggaaac	300
tggtc	ttgcaca	tttgcc	agaacag	atgaaat	gaactatt	360
agaact	ttcagaa	agcaaga	ttgaaa	acactga	cagagagt	420
caaga	ttaggcg	ctggatg	agattgc	agaaag	agaatcat	480
tcttcaa	tgtcaat	aaaccag	attccta	cttttg	tgtttctc	540
catttaa	ttgggac	acctcct	cagggac	gtatga	agctgg	600
acttaca	accaaca	gcagact	actcgga	ccaaca	ttcatgc	660
tcctt	agtcaga	tattcca	gtgcctc	attttgg	caccacc	720
accca	atgcctt	taccaat	tttggc	tcacata	aggttat	780
gtaaa	atgtcta	gatggac	ttcaaa	ctactac	ggtggct	840
gatgc	acccaat	tgattgt	atggtag	gcaattg	aaacaac	900
tttgc	acatgtg	catggat	ctgtgg	ttagca	acaaaa	960
gatttt	ttttgtt	tttga	ccaaa	aaaact	ctttgat	1020
gttatt	ttatcat	ctgtgg	gctacc	taatta	agatgg	1080
tgtttt	acatctg	tgtatt	tgttcag	agtact	taatttg	1140

1181

$\langle 211 \rangle$ 312

<212> PRT

<213> Glycine max

<400> 48

Met Ser Thr Ser Lys Ser Val Ser Ser Ser Ser Glu Asp Asp Asn Glu
1 5 10 15

Leu Arg Arg Gly Pro Trp Thr Leu Glu Glu Asp Asn Leu Leu Ser Gln
20 25 30

Tyr Ile Phe Asn His Gly Glu Gly Arg Trp Asn Leu Leu Ala Lys Arg
35 40 45

Ser Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn
50 55 60

Tyr Leu Lys Pro Asp Val Lys Arg Gly Asn Leu Thr Pro Gln Glu Gln
65 70 75 80

Leu Ile Ile Leu Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser Lys
85 90 95

Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr
100 105 110

Trp Arg Thr Arg Ile Gln Lys Gln Ala Arg His Leu Lys Ile Tyr Thr
115 120 125

Asp Ser Arg Glu Phe Gln Glu Leu Val Arg Arg Phe Trp Met Pro Arg
130 135 140

Leu Leu Gln Lys Ala Lys Glu Ser Ser Ser Ser Asn Met Ser Ile Gln
145 150 155 160

Asn Gln Ala Ile Pro Met Pro Phe Asp Tyr Val Ser Gln His Leu Thr
165 170 175

Val Gly Thr Ile Pro Pro Trp Gln Gly Pro Cys Met Asn Glu Ala Gly
180 185 190

Pro Thr Tyr Met Asp Gln His Glu Gln Thr Gln Thr Arg Asn Thr Asn
195 200 205

Asn Gly Ser Cys Ile Ser Leu Ser Glu Ser Ala Asn Ile Pro Lys Val
210 215 220

Pro Gln His Phe Gly His Thr Thr Ile Thr Gln Phe His Ala Leu Asn
225 230 235 240

Thr Asn Asp Phe Gly Thr Phe Thr Tyr Glu Gly Tyr Asn Val Asn Asn
245 250 255

Asn Val Tyr Glu Met Asp Asn Phe Lys Thr Thr Thr Thr Trp Val Ala
260 265 270

Glu Asp Ala Gln Tyr Pro Ile Gly Asp Cys Gln Met Val Gly Ser Asn
275 280 285

Trp Val Asn Asn Asp Phe Ala Cys Asn Met Trp Asn Met Asp Glu Leu
 290 295 300

Trp Gln Phe Ser Lys Leu Gln Lys
 305 310

<210> 49
 <211> 1186
 <212> DNA
 <213> Glycine max

<400> 49
 aattcggcac gaggccatgt ctacttcaaa gagcgtcagc agttctagtg aagatgacaa 60
 tgaacttaga agagggcctt ggactcttga agaggataat ttgctctccc aatatatttc 120
 tagtcatgga gaagggcgat ggaatttgct agctaaacgt tcaggattaa agcgaactgg 180
 gaaaagttgc agattaaggt ggctaaatta tctaaagcca gatgtaaaac ggggaaattt 240
 aaccccacaa gagcaactta taatcctcga actccactca aagtggggaa acaggtggtc 300
 aaaaattgca caaaatttgc caggcagaaac agacaatgaa atcaagaact attggagaac 360
 taggattcag aaacaagcaa gacatttgaa aattgacact gacaccagag agtttcagga 420
 acttgtagg cgtttctgga tgcctagatg cttcaaaaag cccaagaatc atcttcttca 480
 gccatgtcaa ttcaaaacca ggcaactcct atgccttttg atggtgtttc tcagcattca 540
 actgttggga ccataccatc acattcacac accccttggc agggaccttg tatgaatgaa 600
 gctggtccca cttacatgga ccaacatgag cagaactcag actctgaaca caacaatggg 660
 tcatgcatct ccttgtctga gtcagcaaat tttccaaaag tgcctcagca ttttggacgc 720
 accaccatca cccaatatca tgccttgaat aacaatgact ttggcacctt cacatatgac 780
 ggctacaatg taagcaacaa tgtctatgag atggacaact tcaaaacgcc tactacaagg 840
 gtggctgagg atgcgcaata cccaactggt gattgtcaaa tggtaggaag caattgggta 900
 aacagcgatt ttgcatgtaa catgtggaac atggatgaat tgtggcaatt tagcaagtta 960
 caaaaataag attttagggt ttggtttttt tggagttacc aagactctat ctttgggtgat 1020
 gttattattg ttatcatgaa ctggttgatta gctactacca aattaattaa tacagatggg 1080
 gattgttttc tgtacatctg ttttgcatta ctctgttttg caatttgtat tgattgagaa 1140
 aagtcattaa ttagtcacta gttcaaaaca caaaaaaaaa aaaaaa 1186

<210> 50
 <211> 192
 <212> PRT
 <213> Glycine max

<400> 50
 Met Ser Thr Ser Lys Ser Val Ser Ser Ser Ser Glu Asp Asp Asn Glu
 1 5 10 15
 Leu Arg Arg Gly Pro Trp Thr Leu Glu Glu Asp Asn Leu Leu Ser Gln
 20 25 30
 Tyr Ile Ser Ser His Gly Glu Gly Arg Trp Asn Leu Leu Ala Lys Arg
 35 40 45
 Ser Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn
 50 55 60
 Tyr Leu Lys Pro Asp Val Lys Arg Gly Asn Leu Thr Pro Gln Glu Gln
 65 70 75 80
 Leu Ile Ile Leu Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser Lys
 85 90 95
 Ile Ala Gln Asn Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr
 100 105 110

Trp	Arg	Thr	Arg	Ile	Gln	Lys	Gln	Ala	Arg	His	Leu	Lys	Ile	Asp	Thr
		115					120					125			
Asp	Thr	Arg	Glu	Phe	Gln	Glu	Leu	Val	Arg	Arg	Phe	Trp	Met	Pro	Arg
	130					135					140				
Cys	Phe	Lys	Lys	Pro	Lys	Asn	His	Leu	Leu	Gln	Pro	Cys	Gln	Phe	Lys
145					150					155					160
Thr	Arg	Gln	Leu	Leu	Cys	Leu	Leu	Met	Val	Phe	Leu	Ser	Ile	Gln	Leu
			165						170					175	
Leu	Gly	Pro	Tyr	His	His	Ile	His	Thr	Pro	Leu	Gly	Arg	Asp	Leu	Val
		180						185					190		

<210> 51
 <211> 487
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (358)
 <223> n is a, c, g or t

<220>
 <221> unsure
 <222> (429)
 <223> n is a, c, g or t

<400> 51
 gagaaataaa aagagaagaa agaaaacacg atagtatcat catatcacca ccacacacat 60
 agatagagag aggaaaacga cctatatattt ttttcctttg agagcttcag gggctaggaa 120
 aattagaagg acagccacaa gtataaaggc ggtgaaataa aagagaaaga caagaaggag 180
 acatgggaag accaccttgt tgtgacaaag aaggggtcaa gaaagggcct tggactcctg 240
 aagaagacat catattggtg tcttatattc aggaacatgg tcctggaaat tggagggcag 300
 ttcttgccaa aacaggggtg tcaagatgca gcaagagttg cagacttaga tggacgantt 360
 acctgaggcc aggaatcaag cgtggtaact tcacaagaac aagaggagaa gatgataatc 420
 catcttcang atcttttagg aaacagatgg ggtgcaatag cttcatacct tccacaaagg 480
 acaaggg 487

<210> 52
 <211> 90
 <212> PRT
 <213> Glycine max

<220>
 <221> UNSURE
 <222> (59)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> UNSURE
 <222> (72)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> UNSURE
 <222> (83)
 <223> Xaa can be any naturally occurring amino acid

<400> 52
Met Gly Arg Pro Pro Cys Cys Asp Lys Glu Gly Val Lys Lys Gly Pro
1 5 10 15
Trp Thr Pro Glu Glu Asp Ile Ile Leu Val Ser Tyr Ile Gln Glu His
20 25 30
Gly Pro Gly Asn Trp Arg Ala Val Pro Ala Lys Thr Gly Leu Ser Arg
35 40 45
Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Xaa Tyr Leu Arg Pro Gly
50 55 60
Ile Lys Arg Gly Asn Phe Thr Xaa Glu Gln Glu Glu Lys Met Ile Ile
65 70 75 80
His Leu Xaa Asp Leu Leu Gly Asn Arg Trp
85 90

<210> 53
<211> 1556
<212> DNA
<213> Glycine max

<400> 53
gcacgaggag aaataaaaag agaagaaaga aaacacgata gtatcatcat atcaccacca 60
cacacataga tagagagagg aaaacgacct atattttttt tcctttgaga gcttcagggg 120
ctaggaaaat tagaaggaca gccacaagta taaaggcggg gaaataaaaag agaaagacaa 180
gaaggagaca tgggaagacc accttggtgt gacaaagaag ggggtcaagaa agggccttgg 240
actcctgaag aagacatcat attggtgtct tatattcagg aacatgggtcc tggaaattgg 300
agggcagttc ctgccaaaac aggggtgtca agatgcagca agagttgcag acttagatgg 360
acgaattacc tgaggccagg aatcaagcgt ggtaacttca cagaacaaga ggagaagatg 420
ataatccatc ttcaagatct tttaggaaac agatgggctg caatagcttc ataccttcca 480
caaagaacag acaatgacat aaagaactat tggaataccc atttgagaaa gaagctgaag 540
aagatgcaag caggcgggtga aggtggtagc tttggagaag ggttttcagc ctcaaggcaa 600
atccctagag gccagtggga aagaaggctc caaactgata tccaaatggc aaagagagcc 660
ctcagtgaag ctcttttcacc agagaaaaag ccatcttggt tatctgcctc aaactcaaac 720
ccttcagata gtgacagctc cttctcttcc acaaaaccaa caacaacaca atctgtgtgc 780
tatgcatcaa gtgctgacaa catagctaga atgctcaagg gttggatgaa gaaccaccca 840
aagtccctcaa gaaccaactc gtctatgact cagaactcat tcaacaactt agcaggtgct 900
gatactgctt gtagtagtgg agcaaaggga ccactaagca gtgccgaatt gtctgagaat 960
aattttgaat ccttggttga ttttgatcag tctttggagt cttcaaactc tgatcaattc 1020
tctcagtcct tgtctcctga ggccactgtt ttgcaagatg aaagcaagcc tgatattaat 1080
attgctgcag aaattatgcc cttctctttg cttgagaaat ggctccttga tgaggcaggt 1140
tgccaagaga aattagttgg ttggtgtggt gatgccaagt ttttctaagt tgggttcatt 1200
ttgtgacata tgagactgtg ggattttttt attttatttt attttatttc ataagttata 1260
ggtagggcct catcaattaa tctcgcttcg gccttattag agagagaagt tttccagcct 1320
ttggtgctag acgtgtatat gttaattatt attgacatta tgatgattat tatcatactg 1380
tgttagttgc catacactgg caaacttgct tctcttatgt aaagttgatc ttgcgacgag 1440
atcctgcttt atggcttttag gcagcgcgac cggtcttctc tctttgtgtc gcttgattag 1500
taaccccccc cggggggggg ccgggtccaa atcccccccta atgggggtcct ttttag 1556

<210> 54
<211> 332
<212> PRT
<213> Glycine max

<400> 54
Met Gly Arg Pro Pro Cys Cys Asp Lys Glu Gly Val Lys Lys Gly Pro
1 5 10 15

Trp Thr Pro Glu Glu Asp Ile Ile Leu Val Ser Tyr Ile Gln Glu His
 20 25 30
 Gly Pro Gly Asn Trp Arg Ala Val Pro Ala Lys Thr Gly Leu Ser Arg
 35 40 45
 Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly
 50 55 60
 Ile Lys Arg Gly Asn Phe Thr Glu Gln Glu Lys Met Ile Ile His
 65 70 75 80
 Leu Gln Asp Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu
 85 90 95
 Pro Gln Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr His Leu
 100 105 110
 Arg Lys Lys Leu Lys Lys Met Gln Ala Gly Gly Glu Gly Gly Ser Phe
 115 120 125
 Gly Glu Gly Phe Ser Ala Ser Arg Gln Ile Pro Arg Gly Gln Trp Glu
 130 135 140
 Arg Arg Leu Gln Thr Asp Ile Gln Met Ala Lys Arg Ala Leu Ser Glu
 145 150 155 160
 Ala Leu Ser Pro Glu Lys Lys Pro Ser Cys Leu Ser Ala Ser Asn Ser
 165 170 175
 Asn Pro Ser Asp Ser Ser Ser Ser Phe Ser Ser Thr Lys Pro Thr Thr
 180 185 190
 Thr Gln Ser Val Cys Tyr Ala Ser Ser Ala Asp Asn Ile Ala Arg Met
 195 200 205
 Leu Lys Gly Trp Met Lys Asn Pro Pro Lys Ser Ser Arg Thr Asn Ser
 210 215 220
 Ser Met Thr Gln Asn Ser Phe Asn Asn Leu Ala Gly Ala Asp Thr Ala
 225 230 235 240
 Cys Ser Ser Gly Ala Lys Gly Pro Leu Ser Ser Ala Glu Leu Ser Glu
 245 250 255
 Asn Asn Phe Glu Ser Leu Phe Asp Phe Asp Gln Ser Leu Glu Ser Ser
 260 265 270
 Asn Ser Asp Gln Phe Ser Gln Ser Leu Ser Pro Glu Ala Thr Val Leu
 275 280 285
 Gln Asp Glu Ser Lys Pro Asp Ile Asn Ile Ala Ala Glu Ile Met Pro
 290 295 300
 Phe Ser Leu Leu Glu Lys Trp Leu Leu Asp Glu Ala Gly Cys Gln Glu
 305 310 315 320
 Lys Leu Val Gly Cys Cys Gly Asp Ala Lys Phe Phe
 325 330

<210> 55

<211> 357
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> unsure
 <222> (259)
 <223> n is a, c, g or t

<220>
 <221> unsure
 <222> (307)
 <223> n is a, c, g or t

<220>
 <221> unsure
 <222> (319)
 <223> n is a, c, g or t

<400> 55
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 tttgcgcaaa gtcgcaacaa caaatgtcac ctttgctaata aactttcttc ttgcttcaac 120
 ctctgtaatc tccatgcagg cctcaaccgc acaggaaaga gctgtcgcct ccgggtgggtt 180
 aactacctcc accctgggccc taaagcgtgg gcgcatgact ccccatgaaa gaacgcctca 240
 tcctccaact ccatgctcng tggggaaaca agtgggtccaa ggataacacg gaactgccaa 300
 ggcgtancga caatgaatna aagaactact gggagaacac atttgaggaa aaggaag 357

<210> 56
 <211> 54
 <212> PRT
 <213> Triticum aestivum

<220>
 <221> UNSURE
 <222> (21)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> UNSURE
 <222> (27)..(28)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> UNSURE
 <222> (41)
 <223> Xaa can be any naturally occurring amino acid

<400> 56
 Ala Gly Leu Asn Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Val Asn
 1 5 10 15
 Tyr Leu His Pro Xaa Leu Lys Arg Gly Arg Xaa Xaa Pro Met Lys Glu
 20 25 30
 Arg Leu Ile Leu Gln Leu His Ala Xaa Trp Gly Asn Lys Trp Ser Lys
 35 40 45
 Asp Asn Thr Glu Leu Pro
 50

<210> 57

<211> 1072
 <212> DNA
 <213> Triticum aestivum

<400> 57
 gcacgaggcc aaagtatcag gtttgagggg tgggggatcc aaaaattagg tagctatatt 60
 gaagtatttt gcgcaaagtc gcaacaacaa atgtcacctt tgctaataac tttcttcttg 120
 cttcaacctc tgtaatctcc atgcaggcct caaccgcaca ggaaagagct gtcgcctccg 180
 gtgggttaac tacctccacc ctggcctaaa gcgtgggcgc atgactcccc atgaagaacg 240
 cctcatcctc gagctccatg ctcggtgggg aaacagggtg tccaggatag cacggaagct 300
 gccagggcgt accgacaatg agatcaagaa ctactggaga acacatatga ggaagaaagc 360
 acaggagagg aagaggagcg tgtcaccctc accatcttca tcctcagtga cataccaatc 420
 cattcagcca cagacgccat cgatcatggg aattggcgag caggaacttc atgggtggcag 480
 tagctgcatc acaagcatat tgaagggcac gcctgctgac atggatggat acctcatgga 540
 tcagatatgg atggagattg aggcaccctc tgggggtcaac tttcatgacg ggaaggataa 600
 ttcatacagc agcccctctg gccctctgct gccatcaccg atgtgggatt actacagccc 660
 tgaggcagggc tggaagatgg atgagataaa gatggcccca caagttagct acagtaaagg 720
 aattggcccc agttattgaa gccatatata ttgtatcaga ttactaagtt acttgcaacc 780
 tagcagaagt gaaatgcttt tgttgaaaga accattagca tggatctaaa aaatatattat 840
 atctatctag cattccaagt gtgctcatgt tttatgtatc tactatgtag catctagtgt 900
 gcaagacatg taatgcaagg acacttccac tttgtattca caataatcag ctatctcctg 960
 taagactttt ccaatgcaaa catgattagc aggtgtaata tcaacttaaa tgcttgccaa 1020
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1072

<210> 58
 <211> 198
 <212> PRT
 <213> Triticum aestivum

<400> 58
 Ala Gly Leu Asn Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Val Asn
 1 5 10 15
 Tyr Leu His Pro Gly Leu Lys Arg Gly Arg Met Thr Pro His Glu Glu
 20 25 30
 Arg Leu Ile Leu Glu Leu His Ala Arg Trp Gly Asn Arg Trp Ser Arg
 35 40 45
 Ile Ala Arg Lys Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr
 50 55 60
 Trp Arg Thr His Met Arg Lys Lys Ala Gln Glu Arg Lys Arg Ser Val
 65 70 75 80
 Ser Pro Ser Pro Ser Ser Ser Val Thr Tyr Gln Ser Ile Gln Pro
 85 90 95
 Gln Thr Pro Ser Ile Met Gly Ile Gly Glu Gln Glu Leu His Gly Gly
 100 105 110
 Ser Ser Cys Ile Thr Ser Ile Leu Lys Gly Thr Pro Ala Asp Met Asp
 115 120 125
 Gly Tyr Leu Met Asp Gln Ile Trp Met Glu Ile Glu Ala Pro Ser Gly
 130 135 140
 Val Asn Phe His Asp Gly Lys Asp Asn Ser Tyr Ser Ser Pro Ser Gly
 145 150 155 160
 Pro Leu Leu Pro Ser Pro Met Trp Asp Tyr Tyr Ser Pro Glu Ala Gly

	165		170		175
Trp	Lys Met	Asp Glu Ile Lys Met	Ala Pro Gln Val Ser	Tyr Ser Lys	
	180		185	190	

Gly Ile Gly Pro Ser Tyr
195

<210> 59
<211> 521
<212> DNA
<213> Triticum aestivum

<220>
<221> unsure
<222> (108)
<223> n is a, c, g or t

<220>
<221> unsure
<222> (355)
<223> n is a, c, g or t

<220>
<221> unsure
<222> (361)
<223> n is a, c, g or t

<220>
<221> unsure
<222> (392)
<223> n is a, c, g or t

<220>
<221> unsure
<222> (414)
<223> n is a, c, g or t

<220>
<221> unsure
<222> (431)
<223> n is a, c, g or t

<220>
<221> unsure
<222> (434)
<223> n is a, c, g or t

<220>
<221> unsure
<222> (447)
<223> n is a, c, g or t

<220>
<221> unsure
<222> (456)
<223> n is a, c, g or t

<220>
<221> unsure
<222> (459)

<223> n is a, c, g or t

<400> 59

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cttggatcct ccactagcta cgctcgtccat ggatgtggtg ctgcagagtc gtagcagcaa 60
cagcatggcg gcggagccgg aggaggaggc ggaccggagg aggaggcngg agctccggcg 120
agggccgtgg acggtggacg aggaccttac gctgatcaac tacatcgcg accacggcga 180
gggcccgtgg aacgcgctgg cgcgggccgc cggcctgagg cgcacgggga agagctgccg 240
gctgcggtgg ctgaactacc tccgccccga cgtgaagcgc ggcaacttca ccgccgacga 300
gcagctcctc atcctcgacc tccactctcg ctggggcaac cggtggtcga agatngcgca 360
ncacctcccg ggtcggacgg acaacgaaga tnaaagaact actgggagga ccanggtgca 420
aaaagcacgc naancaactc aactgcnaac tccggaanc gcaaccttta aaggatgcca 480
ataaggtacc tctggatgcc tcgcctctca acgcatcaac c 521
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<210> 60

<211> 131

<212> PRT

<213> Triticum aestivum

<220>

<221> UNSURE

<222> (27)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> UNSURE

<222> (109)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> UNSURE

<222> (111)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> UNSURE

<222> (122)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> UNSURE

<222> (129)

<223> Xaa can be any naturally occurring amino acid

<400> 60

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Met Asp Val Val Leu Gln Ser Arg Ser Ser Asn Ser Met Ala Ala Glu
  1             5             10             15
```

```
Pro Glu Glu Glu Ala Asp Arg Arg Arg Arg Xaa Glu Leu Arg Arg Gly
      20             25             30
```

```
Pro Trp Thr Val Asp Glu Asp Leu Thr Leu Ile Asn Tyr Ile Ala Asp
      35             40             45
```

```
His Gly Glu Gly Arg Trp Asn Ala Leu Ala Arg Ala Ala Gly Leu Arg
      50             55             60
```

```
Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro
      65             70             75             80
```

```
Asp Val Lys Arg Gly Asn Phe Thr Ala Asp Glu Gln Leu Leu Ile Leu
      85             90             95
```

Asp Leu His Ser Arg Trp Gly Asn Arg Trp Ser Lys Xaa Ala Xaa His
100 105 110

Leu Pro Gly Arg Thr Asp Asn Glu Asp Xaa Arg Thr Thr Gly Arg Thr
115 120 125

Xaa Val Gln
130

<210> 61
<211> 464
<212> DNA
<213> Triticum aestivum

<220>
<221> unsure
<222> (435)
<223> n is a, c, g or t

<220>
<221> unsure
<222> (442)
<223> n is a, c, g or t

<220>
<221> unsure
<222> (450)
<223> n is a, c, g or t

<220>
<221> unsure
<222> (457)
<223> n is a, c, g or t

<400> 61
agcgggagcag acgtgagcat ggggaggccg ccgtgctgcg acaaggaggg cgtcaagaag 60
ggcccttgga cgccggagga ggacctcgtg ctgctctcct acgtccagga gcacggcccc 120
ggcaactggc gcgccgtccc caccaggacc ggcctgatgc ggtgtagcaa gagctgccgg 180
ctccggtgga ccaactacct gcgcccaggg atcaagcgcg gcaacttcac cgaccaggag 240
gagaagctca tcgtccacct ccaggcgctg ctcggcaaca ggtgggcccgc gatcgccctcc 300
tacctccccg agcgcaccga caacgacatc aagaactact ggaacacgca actcaagcgc 360
aagctgcaag cggggggcga cgccgcgggc aaaccggcgg cgcaaaggct gctcctcctc 420
aaagggaat ggganaggcg gngcagacgn catcaanatg cgcc 464

<210> 62
<211> 122
<212> PRT
<213> Triticum aestivum

<400> 62
Met Gly Arg Pro Pro Cys Cys Asp Lys Glu Gly Val Lys Lys Gly Pro
1 5 10 15

Trp Thr Pro Glu Glu Asp Leu Val Leu Val Ser Tyr Val Gln Glu His
20 25 30

Gly Pro Gly Asn Trp Arg Ala Val Pro Thr Arg Thr Gly Leu Met Arg
35 40 45

Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly

50 55 60
 Ile Lys Arg Gly Asn Phe Thr Asp Gln Glu Glu Lys Leu Ile Val His
 65 70 75 80
 Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu
 85 90 95
 Pro Glu Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr Gln Leu
 100 105 110
 Lys Arg Lys Leu Gln Ala Gly Gly Asp Ala
 115 120
 <210> 63
 <211> 217
 <212> PRT
 <213> Pisum sativum
 <400> 63
 Met Asp Lys Lys Pro Cys Asn Ser Ser Gln Asp Pro Glu Val Arg Lys
 1 5 10 15
 Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile Ala
 20 25 30
 Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly Leu
 35 40 45
 Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg
 50 55 60
 Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile
 65 70 75 80
 Met Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys
 85 90 95
 His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Arg Thr
 100 105 110
 Arg Ile Gln Lys His Ile Lys Gln Val Asp Asn Pro Asn Gln Gln Asn
 115 120 125
 Phe Gln Gln Lys Met Ser Leu Glu Ile Asn Asp His His His His His
 130 135 140
 Pro His Gln Pro Ser Ser Ser Gln Val Ser Asn Leu Val Glu Pro Met
 145 150 155 160
 Glu Thr Tyr Ser Pro Thr Ser Tyr Gln Gly Thr Leu Glu Pro Phe Pro
 165 170 175
 Thr Gln Phe Pro Thr Ile Asn Asn Asp His His Gln Asn Ser Asn Cys
 180 185 190
 Cys Ala Asn Asp Asn Asn Asn Asn Asn Tyr Trp Ser Met Glu Asp Ile
 195 200 205
 Trp Ser Met Gln Leu Leu Asn Gly Asp
 210 215